Please replace the paragraph beginning at page 55, line 17, with the following:

--Figure 3 summarizes the Pellino-2 gene copy number in various tumors and tumor cell lines. These results were obtained using the quantitative PCR (QPCR) technique. Briefly, probe to Pellino-2 3' untranslated region was designed using PrimerExpress software (Applied Biosystems). This probe set consisting of 3 oligonucleotides (N63226QF: GATGCTGAAGTCGTCTCATTGG (SEQ ID NO:7), N63226QR: CCAGTAGTTTAGCCTTTGTGGCTT (SEQ ID NO:8), N63226QP: [6-FAM]-CGCACAGAAGGAGGCGCATCATAAC-[TAMRA] (SEQ ID NO:9)) was purchased from Operon Technologies (Alameda, CA). Following manufacturer's protocol and the standard curve method as described for Figure 2, the Pellino-2 probe and a reference probe set (TLF7QF: GGTCTCTATTTGCACTTGGCTGAT (SEQ ID NO:10), TLF7QR: TTTTCATTGTTGACCAAGCTAGACA (SEQ ID NO:11), TLF7QP: [6-FAM]-TAGGGCATACTGCCTGCATATTTCCTGCT-[TAMRA] (SEQ ID NO:12)) representing single copy region in the human genome were used to determine the Pellino-2 gene copy number in tumor DNAs using Taqman 7700 sequence detector (Applied Biosytems).--

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 19, at the end of the application.

REMARKS

Although the nucleic acid sequence for Pellino 1 was assigned SEQ ID NO:1 (see page 5, lines 16 and 17; page7, lines 29 and 30; page 23, lines 5 and 6; and page 25, lines 20 and 21), the Specification does not contain the actual sequence. The Sequence Listing contains the nucleic acid sequence for human Pellino 1 found in GenBank under Accession No. AF302505.1, as described on page 5, lines 16-17, and

page 23, lines 5 and 6 of the Specification, the former instance specifically naming as SEQ ID NO:1 the GenBank Accession No. AF302505.1 entry.

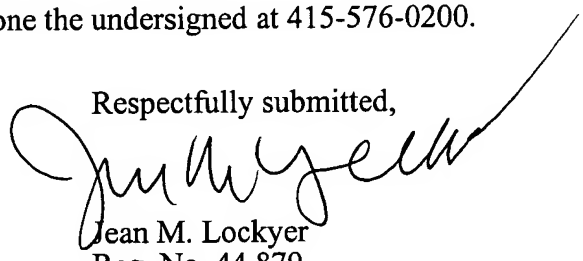
Applicants request entry of this amendment in adherence with 37 C.F.R. §§1.821 to 1.825. This amendment is accompanied by a floppy disk containing the above named sequences, SEQ ID NOS:1-42, in computer readable form, and a paper copy of the sequence information which has been printed from the floppy disk.

The information contained in the computer readable disk was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy. This amendment contains no new matter.

Attached hereto is a marked-up version of the changes made to the Specification by the current Amendment. The attached pages are captioned "**VERSION WITH MARKINGS TO SHOW CHANGES MADE.**"

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,



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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Paragraph beginning at line 29 of page 4 has been amended as follows:

Figure 1 shows a comparison of Pellino 1 (SEQ ID NO:2) and Pellino 2 (SEQ ID NO:4) amino acids sequences. The two sequences exhibit approximately 81% amino acid identity (amino acid sequence identity = SEQ ID NOS:13-42).

Paragraph beginning at line 12 of page 54 has been amended as follows:

Four nano-grams of Clontech Human Universal Quick-Clone cDNA (product # 7109-1) was mixed in a total volume of 50 µL with these ingredients: 200 µM dNTP, oligonucleotides PELD1 and PELD2 (PELD1 = ATGTTTTCCCCTGGCCAGGAGGAACAC (SEQ ID NO:5), PELD2 = TCAGTCAATTGGACCTTGGAAAATTAA (SEQ ID NO:6); 0.5 µM each), ~~(PELD1= ATGTTTTCCCCTGGCCAGGAGGAACAC, PELD2=TCAGTCAATTGGACCTTGGAAAATTAA; 0.5 µM each),~~ 20 mM Tris-HCl pH 8.85, 6 mM $(NH_4)_2SO_4$, 10 mM KCl, 2 mM $MgSO_4$, 0.1% Triton-X-100, 10 µg/mL nuclease-free bovine serum albumin, and 3 units of pfu-turbo DNA polymerase (Stratagene, La Jolla, CA). The reaction was then overlaid with mineral oil (30 µL) and amplified using a PCR thermal cycler (MJ Research, Watertown, MA) for 40 cycles where each cycle consists of 3 steps: 95°C for 20 sec, 59°C for 30 sec, and 72°C for 1.5 min. Subsequently, the mixture was purified using High-Pure PCR purification columns (Roche, Indianapolis, IN) following manufacturer's recommendation. Upon analyses using 2% agarose gel electrophoresis, a product of approximately 1.3 kb in length was detected, representing the full-length open reading frame of Pellino-2.

Paragraph beginning at line 17 of page 55 has been amended as follows:

Figure 3 summarizes the Pellino-2 gene copy number in various tumors and tumor cell lines. These results were obtained using the quantitative PCR (QPCR) technique. Briefly, probe to Pellino-2 3' untranslated region was designed using PrimerExpress software (Applied Biosystems). This probe set consisting of 3 oligonucleotides (N63226QF: GATGCTGAAGTCGTCTCATTGG (SEQ ID NO:7), N63226QR: CCAGTAGTTTAGCCTTTGTGGCTT (SEQ ID NO:8), N63226QP: [6-FAM]-CGCACAGAAGGAGGCGCATCATAAC-[TAMRA] (SEQ ID NO:9)) was purchased from Operon Technologies (Alameda, CA). Following manufacturer's protocol and the standard curve method as described for Figure 2, the Pellino-2 probe and a reference probe set (TLF7QF: GGTCTCTATTTGCACTTGGCTGAT (SEQ ID NO:10), TLF7QR: TTTTCATTGTTGACCAAGCTAGACA (SEQ ID NO:11), TLF7QP: [6-FAM]-TAGGGCATACTGCCTGCATATTTCCTGCT-[TAMRA] (SEQ ID NO:12)) representing single copy region in the human genome were used to determine the Pellino-2 gene copy number in tumor DNAs using Taqman 7700 sequence detector (Applied Biosytems).